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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/975,072

DATE: 10/29/2001

TIME: 16:16:19

Input Set : A:\269conversion.txt

Output Set: N:\CRF3\10292001\I975072.raw

3 <110> APPLICANT: Roch, Jean-Marc
4 Bartel, Paul L.
5 Heichman, Karen
7 <120> TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
8 Diseases
10 <130> FILE REFERENCE: Protein Interactions in ND
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/975,072
C--> 13 <141> CURRENT FILING DATE: 2001-10-12
15 <150> PRIOR APPLICATION NUMBER: US 60/240,790
16 <151> PRIOR FILING DATE: 2000-10-17
18 <160> NUMBER OF SEQ ID NOS: 4
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 40
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence:tail for
29 forward primer for yeast two-hybrid system
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32 gcaggaaaca gctatgacca tacagtcagc ggccgccacc 40
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 39
37 <212> TYPE: DNA
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41 <223> OTHER INFORMATION: Description of Artificial Sequence:tail for
42 reverse primer for yeast two-hybrid system
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48 <210> SEQ ID NO: 3
49 <211> LENGTH: 2740
50 <212> TYPE: DNA
51 <213> ORGANISM: Homo sapiens
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (217)..(1332)
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60 cgacggagaa ggcactctta ttaccgacc aagaaagctc ctccccgctc ctccgttagc 120
62 taattaaaac atttttcagg gacgtagcca tccagagaca ttccattatt gttccattga 180
64 cctttccctc atcactgagt cctttggagc tgagtt atg tca aca gct gcc tta 234
65 Met Ser Thr Ala Ala Leu
66 1 5
68 att act ttg gtc aga agt ggt ggg aac cag gtg aga agg aga gtg ctg 282
69 Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu
70 10 15 20

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72 cta agc tcc cgc ctg ctg cag gac gac agg cgg gtg aca ccc acg tgc 330
73 Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys
74      25      30      35
76 cac agc tcc act tca gag cct agg tgt tct cgg ttt gac cca gat ggt 378
77 His Ser Ser Thr Ser Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly
78      40      45      50
80 agt ggg agt cca gct acc tgg gac aat ttt ggg atc tgg gat aac cgc 426
81 Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Asn Arg
82 55      60      65      70
84 att gat gag cca att ctg ctg cca ccc agc att aag tat ggc aag cca 474
85 Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro
86      75      80      85
88 att ccc aaa atc agc ttg gaa aat gtg ggg tgc gcc tca cag att ggc 522
89 Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly
90      90      95      100
92 aaa cgg aaa gag aat gaa gat cgg ttt gac ttc gct cag ctg aca gat 570
93 Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp
94      105      110      115
96 gag gtc ctg tac ttt gca gtg tat gat gga cac ggt gga cct gca gca 618
97 Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly His Gly Gly Pro Ala Ala
98      120      125      130
100 gct gat ttc tgt cat acc cac atg gag aaa tgt att atg gat ttg ctt 666
101 Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu
102 135      140      145      150
104 cct aag gag aag aac ttg gaa act ctg ttg acc ttg gct ttt cta gaa 714
105 Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu Thr Leu Ala Phe Leu Glu
106      155      160      165
108 ata gat aaa gcc ttt tcg agt cat gcc cgc ctg tct gct gat gca act 762
109 Ile Asp Lys Ala Phe Ser Ser His Ala Arg Leu Ser Ala Asp Ala Thr
110      170      175      180
112 ctt ctg acc tct ggg act act gca aca gta gcc cta ttg cga gat ggt 810
113 Leu Leu Thr Ser Gly Thr Thr Ala Thr Val Ala Leu Leu Arg Asp Gly
114      185      190      195
116 att gaa ctg gtt gta gcc agt gtt ggg gac agc cgg gct att ttg tgt 858
117 Ile Glu Leu Val Val Ala Ser Val Gly Asp Ser Arg Ala Ile Leu Cys
118      200      205      210
120 aga aaa gga aaa ccc atg aag ctg acc att gac cat act cca gaa aga 906
121 Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg
122 215      220      225      230
124 aaa gat gaa aaa gaa agg atc aag aaa tgt ggt ggt ttt gta gct tgg 954
125 Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys Gly Gly Phe Val Ala Trp
126      235      240      245
128 aat agt ttg ggg cag cct cac gta aat ggc agg ctt gca atg aca aga 1002
129 Asn Ser Leu Gly Gln Pro His Val Asn Gly Arg Leu Ala Met Thr Arg
130      250      255      260
132 agt att gga gat ttg gac ctt aag acc agt ggt gtc ata gca gaa cct 1050
133 Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser Gly Val Ile Ala Glu Pro
134      265      270      275
136 gaa act aag agg att aag tta cat cat gct gat gac agc ttc ctg gtc 1098

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137 Glu Thr Lys Arg Ile Lys Leu His His Ala Asp Asp Ser Phe Leu Val
138      280                      285                      290
140 ctc acc aca gat gga att aac ttc atg gtg aat agt caa gag att tgt 1146
141 Leu Thr Thr Asp Gly Ile Asn Phe Met Val Asn Ser Gln Glu Ile Cys
142 295                      300                      305                      310
144 gac ttt gtc aat cag tgc cat gat ccc aac gaa gca gcc cat gcg gtg 1194
145 Asp Phe Val Asn Gln Cys His Asp Pro Asn Glu Ala Ala His Ala Val
146                      315                      320                      325
148 act gaa cag gca ata cag tac ggt act gag gat aac agt act gca gta 1242
149 Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu Asp Asn Ser Thr Ala Val
150                      330                      335                      340
152 gta gtg cct ttt ggt gcc tgg gga aaa tat aag aac tct gaa atc aac 1290
153 Val Val Pro Phe Gly Ala Trp Gly Lys Tyr Lys Asn Ser Glu Ile Asn
154                      345                      350                      355
156 ttc tca ttc agc aga agc ttt gcc tcc agt gga cga tgg gcc 1332
157 Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser Gly Arg Trp Ala
158      360                      365                      370
160 tgattaccag ctgggactta gattttctgt gcaacagttt ttcactgagc atgtcaagaa 1392
162 actgataaga tcaaaaaggt ctccctaactc actagatcag cgcacaagtc agtgtaaacc 1452
164 acttagatag tagttttttc ataaatgctc atcatattta tgttccgctg tacatgttca 1512
166 gtataaatat atgtgtagtg aagctactgt gagtctttta atggaaagag caaatgagaa 1572
168 gtggtttgga tacacttgat gagagatgag agtgtcacat taataatttt taagactcct 1632
170 aggcagctat gggtttcttt tgatcatttt tgttctttat tcatttgaac acgtttttga 1692
172 agttcttcaa aactagtcat tttgaatttt gacagctatt caatatgtga tctccaagtt 1752
174 taaaaaaatt tttttccaga ctccctaatt cctaaaaatgc gaggttttat ttttaataac 1812
176 tgtaccaagg aataagtatg aaacagtttc tctgttacca tattttgtat tctggaccac 1872
178 ttactggtga aagcaaccat gcaaaagaaa ttaatttggtc caggcacagt ggctcatgcc 1932
180 tgtaatccca aattgctggg attacagcac tgtgccctcc taggaaatta ttttttaagt 1992
182 gaaattttat ttttattttt tttaggattt tggtagagaa tgagtaggcc tactcatcaa 2052
184 tatcaaacag gacatttagt ttctttcctt agaacagaca taaatttaat ttcatggtaa 2112
186 tatgataata agaaaatgct tctatttttc tttagcacct ccatggttct catataccca 2172
188 tgtctgtaaa aagtgcacat agaattttgt tgggttacat tttattgtat ttattagatt 2232
190 cgcttatata gatgacttag gcagaaataa agtcatgtct ttagaagggtg aacaagccaa 2292
192 cttgtgatgg cctgcctttt gcttttgcca gttgggatga gaacaattga ctctccatt 2352
194 ggttggttaga tagttgaaat ggtgcgttgg tggtcatact tagtgttcta ggctgtgaaa 2412
196 tcatggagtt cttccacttc caagaatgac tcatttgctg ttggattcta gtacagaatt 2472
198 tagcagcctg atgtgtcccc aaactgattt aattttctact gaagtgcctt tgtgtacatt 2532
200 tgttttgtaa tttaccaaag tactacctga gtgtataatg actcctgcag tgagttaatg 2592
202 taattgctgc tttgaccatt gttttaaatc tgtgtactag agtaactgtg agcagaatga 2652
204 aatcacatta tctcagtgtt caaaatatca ttctaataaa gtacatgcat taaacaattt 2712
206 taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2740
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210 <211> LENGTH: 372
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
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216 1 5 10 15
218 Val Arg Arg Arg Val Leu Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg

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219		20		25		30
221	Arg Val Thr	Pro Thr Cys His Ser	Ser Thr Ser Glu	Pro Arg Cys Ser		
222	35	40	45			
224	Arg Phe Asp	Pro Asp Gly Ser Gly	Ser Pro Ala Thr	Trp Asp Asn Phe		
225	50	55	60			
227	Gly Ile Trp	Asp Asn Arg Ile Asp	Glu Pro Ile Leu	Leu Pro Pro Ser		
228	65	70	75	80		
230	Ile Lys Tyr	Gly Lys Pro Ile Pro	Lys Ile Ser Leu	Glu Asn Val Gly		
231	85	90	95			
233	Cys Ala Ser	Gln Ile Gly Lys Arg	Lys Glu Asn Glu	Asp Arg Phe Asp		
234	100	105	110			
236	Phe Ala Gln	Leu Thr Asp Glu	Val Leu Tyr Phe	Ala Val Tyr Asp Gly		
237	115	120	125			
239	His Gly Gly	Pro Ala Ala Ala	Asp Phe Cys His	Thr His Met Glu Lys		
240	130	135	140			
242	Cys Ile Met	Asp Leu Leu Pro	Lys Glu Lys Asn	Leu Glu Thr Leu Leu		
243	145	150	155	160		
245	Thr Leu Ala	Phe Leu Glu Ile	Asp Lys Ala Phe	Ser Ser His Ala Arg		
246	165	170	175			
248	Leu Ser Ala	Asp Ala Thr Leu	Leu Thr Ser Gly	Thr Thr Ala Thr Val		
249	180	185	190			
251	Ala Leu Leu	Arg Asp Gly Ile	Glu Leu Val Val	Ala Ser Val Gly Asp		
252	195	200	205			
254	Ser Arg Ala	Ile Leu Cys Arg	Lys Gly Lys Pro	Met Lys Leu Thr Ile		
255	210	215	220			
257	Asp His Thr	Pro Glu Arg Lys	Asp Glu Lys Glu	Arg Ile Lys Lys Cys		
258	225	230	235	240		
260	Gly Gly Phe	Val Ala Trp Asn	Ser Leu Gly Gln	Pro His Val Asn Gly		
261	245	250	255			
263	Arg Leu Ala	Met Thr Arg Ser	Ile Gly Asp Leu	Asp Leu Lys Thr Ser		
264	260	265	270			
266	Gly Val Ile	Ala Glu Pro Glu	Thr Lys Arg Ile	Lys Leu His His Ala		
267	275	280	285			
269	Asp Asp Ser	Phe Leu Val Leu	Thr Thr Asp Gly	Ile Asn Phe Met Val		
270	290	295	300			
272	Asn Ser Gln	Glu Ile Cys Asp	Phe Val Asn Gln	Cys His Asp Pro Asn		
273	305	310	315	320		
275	Glu Ala Ala	His Ala Val Thr	Glu Gln Ala Ile	Gln Tyr Gly Thr Glu		
276	325	330	335			
278	Asp Asn Ser	Thr Ala Val Val	Val Pro Phe Gly	Ala Trp Gly Lys Tyr		
279	340	345	350			
281	Lys Asn Ser	Glu Ile Asn Phe	Ser Phe Ser Arg	Ser Phe Ala Ser Ser		
282	355	360	365			
284	Gly Arg Trp	Ala				
285	370					

VERIFICATION SUMMARY

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Output Set: N:\CRF3\10292001\I975072.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date